

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/719, 624
Source: TFWJ
Date Processed by STIC: 11-18-04

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RAW SEQUENCE LISTING DATE: 11/15/2004
PATENT APPLICATION: US/10/719,024 TIME: 15:02:37

Input Set : D:\US Utility 50229-420 Sequence Listing.txt
Output Set: N:\CRF4\11152004\J719024.raw

3 <110> APPLICANT: University of Kentucky Research Foundation
4 JONES, Grace
5 JONES, Davy
7 <120> TITLE OF INVENTION: MUTANTS AND ASSAY SYSTEM TO IDENTIFY USP/RXR LIGANDS
9 <130> FILE REFERENCE: 050229-0420
11 <140> CURRENT APPLICATION NUMBER: 10/719,024
12 <141> CURRENT FILING DATE: 2003-11-24
14 <150> PRIOR APPLICATION NUMBER: 60/428,282
15 <151> PRIOR FILING DATE: 2002-11-22
17 <160> NUMBER OF SEQ ID NOS: 23
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2488
23 <212> TYPE: DNA
24 <213> ORGANISM: Drosophila melanogaster
26 <400> SEQUENCE: 1
27 aaaaaatgtcg acgcgaaaaa aggtatttat tcattagtca gaaagtctgg cattctttgt 60
29 ttgttggtaa aaagcgaat tgtttggagg cgagcgaata aagtgcgctg ctccatcgcc 120
31 tcaagattat gtaaatgcag caacgacccc accaacaacg aaactgcaac ctgctccact 180
33 tggcccaacg gaccaatagc ggacggacgg acacgggtgc gttggcaaag tgaaacccca 240
35 acagagaggc gaaagcggc caagacacac cacatacaca cgaagagaac gagcaagaag 300
37 aaaccggtag gcgaggagg cgctgccccca atatacccg caccacatca 360
39 caagccagg atggacaact gcgaccaggcg cggcagctt cggtctgagcc acatcaagga 420
41 ggaggtcaag cggacatct cgcagctgaa cgacagcaac aacagcagct tttcgcccaa 480
43 ggccgagagt cccgtgcct tcatgcaggc catgtccatg gtccacgtgc tgccggctc 540
45 caactccgccc agctccaaca acaacagcgc tggagatgcc caaatggcgc aggcgcccaa 600
47 ttcggctgga ggctctgccc cgcgtcgcagt ccagcagcag tatccgccta accatccgct 660
49 gagccgcagc aagcacctct getctatttg cggggatcgg gccagtggca agcactacgg 720
51 cgtgtacagc tggagggtct gcaagggtct ctttaaacgc acagtgcgcgca aggatctcac 780
53 atacgcttgc agggagaacc gcaactgcatt catagacaag cggcagagga accgctgcca 840
55 gtactgccgc taccagaagt gcctaaccctg cggcatgaag cgcgaagcgg tccaggagga 900
57 gcgtaacgc ggcggccca atgcggcggg taggctcagc gccagcggag gccggcagtag 960
59 cggtccaggc tggtaggcg gatccagctc tcaaggcggaa ggaggaggag gccggcgtttc 1020
61 tggcggaaatg ggcagcggca acggttctga tgacttcatg accaatagcg tggccaggga 1080
63 tttctcgatc gagcgcattca tagaggccga gcagcggcg gagacccaaat gccggcgtatcg 1140
65 tgcactgacg ttccctgcgcg ttggccctta ttccacagtc cagccggact acaagggtgc 1200
67 cgtgtccggc ctgtgccaag tggtaaccaa acagctttc cagatggtcg aatacgcgcg 1260
69 catgatgccg cactttgccc aggtgccgct ggacgaccag gtgattctgc tgaaagccgc 1320
71 ttggatcgag ctgctcattt cgaacgtggc ctggatcgacg atcgtttcgc tggatgacgg 1380
73 cggtccggc ggcggggcgt gtggactagg ccacatggc tccttgcgc gacgatcacc 1440
75 gggccttcag cccccagcaggc tggtaaccaa ccagatctc tggatcaccatc gcaacagtgc 1500
77 gatcaaagcc ggtgtgtcag ccatcttcga ccgcatttg tggagctga gtgtaaagat 1560
79 qaaqcqqctq aatctcgacc qacqcgqaqct qtccctgctt aaggccatca tactgtacaa 1620
CPG.6

(pg. 6)

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81	cccgacata	cgcggatca	agagccggc	ggagatcgag	atgtccgcg	agaagggtgt	1680
83	cgctgcctg	gacgagcact	gccgcctgga	acatccggc	gacgtggac	gcttcgcgc	1740
85	actgctgcgt	cgtctgccc	cttgcgatc	gatcagcctg	aagtccagg	atcaccttt	1800
87	cctctccgc	attaccagcg	accggccgt	ggaggagctc	tttctcgagc	agctggaggc	1860
89	gccgcgc	cccgccctgg	cgatgaaact	ggagtaggg	ccgcactcta	aagtctccc	1920
91	cgttctccat	ccgaaaaat	tttcattgtg	attgcgttt	tttgcatttc	tcctcttat	1980
93	cccttataacc	ctacaaaagc	cccctaata	tacgcaaaat	gtgtatgtaa	ttgtttattt	2040
95	ttttttattt	acctaata	attattatta	ttgatata	aaatgtttt	cttaagatga	2100
97	agattagcct	cctcgacgt	tatgtcccag	taaaacaaaa	acaaacaaaa	tccaaaactt	2160
99	gaaaagaaca	caaaacacga	acgagaaaat	gcacacaagc	aaagtaaaag	taaaagttaa	2220
101	actaaagcta	aacgagtaaa	gatattaaa	taacggtaa	aattaatgca	tagttatgat	2280
103	ctacagacgt	atgtaaacat	acaaattcag	cataaaatata	tatgtcagca	ggcgcata	2340
105	tgcgtgtctg	gccccgttct	aaatcaattt	taattacttt	ttaacataaa	tttacccaaa	2400
107	acgttatcaa	ttagatgcga	gataaaaaaa	tcaccgacga	aaaccaacaa	aatatatatcta	2460
109	tgtataaaaaa	atataaactg	cataacaa				2488
112	<210>	SEQ ID NO:	2				
113	<211>	LENGTH:	508				
114	<212>	TYPE:	PRT				
115	<213>	ORGANISM:	Drosophila melanogaster				
117	<400>	SEQUENCE:	2				
119	Met	Asp	Asn	Cys	Asp	Asp	1680
120	1			5		10	1740
123	Glu	Glu	Val	Lys	Pro	Asp	1800
124				20		25	1860
127	Ser	Phe	Ser	Pro	Lys	Ala	1920
128				35		40	1980
131	Ser	Met	Val	His	Val	Leu	2040
132		50			55		2100
135	Asn	Ser	Ala	Gly	Asp	Ala	2160
136	65			70		75	2220
139	Gly	Ser	Ala	Ala	Ala	Val	2280
140					85		2340
143	Leu	Ser	Gly	Ser	Lys	His	2400
144		100			105		2460
147	Gly	Lys	His	Tyr	Gly	Val	2488
148		115			120		
151	Lys	Arg	Thr	Val	Arg	Lys	
152		130			135		
155	Asn	Cys	Ile	Ile	Asp	Lys	
156		145			150		
159	Tyr	Gln	Lys	Cys	Leu	Thr	
160		160			165		
163	Glu	Arg	Gln	Arg	Gly	Ala	
164		180			185		
167	Gly	Gly	Gly	Ser	Ser	Gly	
168		195			200		
171	Gly	Gly	Gly	Gly	Gly	Val	
172		210			215		
175	Gly	Ser	Asp	Asp	Phe	Met	
						Thr	
						Asn	
						Ser	
						Val	
						Ser	
						Arg	
						Asp	
						Phe	
						Ser	
						Ile	

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176	225	230	235	240
179	Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp			
180	245	250	255	
183	Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro			
184	260	265	270	
187	Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln			
188	275	280	285	
191	Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln			
192	290	295	300	
195	Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu			
196	305	310	315	320
199	Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp			
200	325	330	335	
203	Gly Gly Ala Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe			
204	340	345	350	
207	Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln			
208	355	360	365	
211	Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala			
212	370	375	380	
215	Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu			
216	385	390	395	400
219	Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr			
220	405	410	415	
223	Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys			
224	420	425	430	
227	Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His			
228	435	440	445	
231	Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Pro Ala			
232	450	455	460	
235	Leu Arg Ser Ile Ser Leu Lys Cys Gln Asp His Leu Phe Leu Phe Arg			
236	465	470	475	480
239	Ile Thr Ser Asp Arg Pro Leu Glu Leu Phe Leu Glu Gln Leu Glu			
240	485	490	495	
243	Ala Pro Pro Pro Gly Leu Ala Met Lys Leu Glu			
244	500	505		
247	<210> SEQ ID NO: 3			
248	<211> LENGTH: 61			
249	<212> TYPE: DNA			
250	<213> ORGANISM: Trichoplusia ni granulovirus			
252	<400> SEQUENCE: 3			
253	gaccaattaa taggtgacct gcgataaaaa ttacctataa atatgtgatg ttgctggatt	60		
255	g	61		
258	<210> SEQ ID NO: 4			
259	<211> LENGTH: 134			
260	<212> TYPE: DNA			
261	<213> ORGANISM: Trichoplusia ni granulovirus			
263	<400> SEQUENCE: 4			
264	cgagaggta tcgccccata caacaacaat gataatgacg tgcaagcaga taatagtgaa	60		
266	aaaataacag atactagagt ataaaaaggg gatgctggga gtggacaggc acagtcgtgg	120		

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PATENT APPLICATION: US/10/719,024

DATE: 11/15/2004

TIME: 15:02:37

Input Set : D:\US Utility 50229-420 Sequence Listing.txt
 Output Set: N:\CRF4\11152004\J719024.raw

268 tgtggcagca aaca 134
 271 <210> SEQ ID NO: 5
 272 <211> LENGTH: 69
 273 <212> TYPE: DNA
 274 <213> ORGANISM: Trichoplusia ni granulovirus
 276 <400> SEQUENCE: 5
 277 tcagttaaa aagggtgc ttctcgtaa gagtacagtt gaactcacat cgagttaact 60
 279 ccacgatga 69
 282 <210> SEQ ID NO: 6
 283 <211> LENGTH: 63
 284 <212> TYPE: DNA
 285 <213> ORGANISM: Trichoplusia ni granulovirus
 287 <400> SEQUENCE: 6
 288 taagggttgtt ataaaaaggc gatcaatcat tgacaaacag tttgcagcag gctgtggaa 60
 290 cga 63
 293 <210> SEQ ID NO: 7
 294 <211> LENGTH: 15
 295 <212> TYPE: DNA
 296 <213> ORGANISM: Artificial Sequence
 298 <220> FEATURE:
 299 <223> OTHER INFORMATION: Chemically synthesized
 301 <400> SEQUENCE: 7 15
 302 gaggtcaatg acctc
 305 <210> SEQ ID NO: 8
 306 <211> LENGTH: 24
 307 <212> TYPE: DNA
 308 <213> ORGANISM: Artificial Sequence
 310 <220> FEATURE:
 311 <223> OTHER INFORMATION: Chemically synthesized
 314 <220> FEATURE:
 315 <221> NAME/KEY: misc_feature
 316 <222> LOCATION: (7)..(18)
 317 <223> OTHER INFORMATION: N is A, T, G or C
 319 <220> FEATURE:
 320 <221> NAME/KEY: misc_feature
 321 <222> LOCATION: (8)..(18)
 322 <223> OTHER INFORMATION: Any one of these 11 N's may or may not be present
 324 <400> SEQUENCE: 8 24
 W--> 325 aggtcannnn nnnnnnnnnag gtca
 328 <210> SEQ ID NO: 9
 329 <211> LENGTH: 24
 330 <212> TYPE: DNA
 331 <213> ORGANISM: Artificial Sequence
 333 <220> FEATURE:
 334 <223> OTHER INFORMATION: Chemically synthesized
 337 <220> FEATURE:
 338 <221> NAME/KEY: misc_feature
 339 <222> LOCATION: (7)..(18)
 340 <223> OTHER INFORMATION: N = A, T, G or C

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 Output Set: N:\CRF4\11152004\J719024.raw

342 <220> FEATURE:
 343 <221> NAME/KEY: misc_feature
 344 <222> LOCATION: (8)..(18)
 345 <223> OTHER INFORMATION: Any one of these 11 N's may or may not be present
 347 <400> SEQUENCE: 9

24

W--> 348 tgacctnnnn nnnnnnnntg acct
 351 <210> SEQ ID NO: 10
 352 <211> LENGTH: 13
 353 <212> TYPE: DNA
 354 <213> ORGANISM: Artificial Sequence
 356 <220> FEATURE:
 357 <223> OTHER INFORMATION: Chemically synthesized
 360 <220> FEATURE:
 361 <221> NAME/KEY: misc_feature
 362 <222> LOCATION: (7)..(7)
 363 <223> OTHER INFORMATION: n is a, c, g, or t
 365 <400> SEQUENCE: 10

13

W--> 366 aggtcanagg tca
 369 <210> SEQ ID NO: 11
 370 <211> LENGTH: 26
 371 <212> TYPE: DNA
 372 <213> ORGANISM: Artificial Sequence
 374 <220> FEATURE:
 375 <223> OTHER INFORMATION: Chemically synthesized
 378 <220> FEATURE:
 379 <221> NAME/KEY: misc_feature
 380 <222> LOCATION: (7)..(7)
 381 <223> OTHER INFORMATION: n is a, c, g, or t
 383 <220> FEATURE:
 384 <221> NAME/KEY: misc_feature
 385 <222> LOCATION: (20)..(20)
 386 <223> OTHER INFORMATION: n is a, c, g, or t
 388 <400> SEQUENCE: 11

26

W--> 389 aggtcanagg tcaagg tcan aggtca
 392 <210> SEQ ID NO: 12
 393 <211> LENGTH: 26
 394 <212> TYPE: DNA
 395 <213> ORGANISM: Artificial Sequence
 397 <220> FEATURE:
 398 <223> OTHER INFORMATION: Chemically synthesized
 401 <220> FEATURE:
 402 <221> NAME/KEY: misc_feature
 403 <222> LOCATION: (7)..(7)
 404 <223> OTHER INFORMATION: n is a, c, g, or t
 406 <220> FEATURE:
 407 <221> NAME/KEY: misc_feature
 408 <222> LOCATION: (20)..(20)
 409 <223> OTHER INFORMATION: n is a, c, g, or t
 411 <400> SEQUENCE: 12

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/15/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18
Seq#:9; N Pos. 1, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18
Seq#:10; N Pos. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18
Seq#:11; N Pos. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18
Seq#:12; N Pos. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20
Seq#:16; N Pos. 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20

VERIFICATION SUMMARY

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L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0